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Light affects fumonisin production in strains of *Fusarium fujikuroi*, *Fusarium proliferatum*, and *Fusarium verticillioides* isolated from rice

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22 **Light affects fumonisin production in strains of *Fusarium fujikuroi*, *Fusarium***
23 ***proliferatum*, and *Fusarium verticillioides* isolated from rice**

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38 **ABSTRACT**

39

40 Three *Fusarium* species associated to bakanae disease of rice (*Fusarium fujikuroi*, *Fusarium*
41 *proliferatum*, and *Fusarium verticillioides*) were investigated for their ability to produce fumonisins
42 (FB₁ and FB₂) under different light conditions, and for pathogenicity. The conditions that highly
43 stimulated the fumonisin production compared to darkness were yellow and green light in *F.*
44 *verticillioides* strains; white and blue light, and light/dark alternation in *F. fujikuroi* and *F.*
45 *proliferatum* strains. In general, all light conditions influenced positively the fumonisin production
46 with respect to the dark. Expression of the *FUM1* gene, which is necessary for initiation of
47 fumonisin production, was in accordance with the fumonisin biosynthetic profile. High and low
48 fumonisin-producing *F. fujikuroi* strains showed typical symptoms of bakanae disease, abundant
49 fumonisin-producing *F. verticillioides* strains exhibited chlorosis and stunting of rice plants, while
50 fumonisin-producing *F. proliferatum* strains were asymptomatic on rice. We report that *F. fujikuroi*
51 might be an abundant fumonisin producer with levels comparable to that of *F. verticillioides* and *F.*
52 *proliferatum*, highlighting the need of deeper mycotoxicological analyses on rice isolates of *F.*
53 *fujikuroi*. Our results showed for the first time the influence of light on fumonisin production in
54 isolates of *F. fujikuroi*, *F. proliferatum*, and *F. verticillioides* from rice.

55

56 *Keywords:* Bakanae disease; Rice; *Fusarium*; Pathogenicity; FB₁; FB₂

57 1. Introduction

58

59 The fungal genus *Fusarium* is composed of a large number of species that can be pathogenic on
60 plants. *Fusarium* species are causal agents of various diseases affecting many economically
61 important cereals, such as rice (*Oryza sativa* L.). *Fusarium fujikuroi* Nirenberg [teleomorph
62 *Gibberella fujikuroi* (Sawada) Ito in Ito & K. Kimura] is an important rice pathogen, causing the
63 bakanae disease or disease of foolish seedlings (Carter et al., 2008; Desjardins et al., 1997), and is a
64 member of the polyphyletic taxon *Gibberella fujikuroi* species complex (GFSC; O'Donnell et al.,
65 1998a). Beside *F. fujikuroi* other *Fusarium* species, such as *Fusarium proliferatum* and *Fusarium*
66 *verticillioides*, have been associated with bakanae disease on rice (Desjardins et al., 2000; Nur Ain
67 Izzati and Salleh, 2010; Wulff et al., 2010).

68 *Fusarium* spp. produce a wide range of biologically active secondary metabolites, among them
69 there are mycotoxins which are harmful to animals and humans (Desjardins and Proctor, 2007), and
70 they are considered the most important toxigenic fungi in the Northern temperate areas (Gutleb et
71 al., 2002). Fumonisin are an important class of *Fusarium* mycotoxins. Among the *Fusarium* spp.
72 isolated from rice, *F. verticillioides* and *F. proliferatum* are reported as the most abundant
73 fumonisin producers, whereas *F. fujikuroi*, the causal agent of the bakanae disease, has a lower
74 capacity of fumonisin production (Stępień et al., 2011; Wulff et al., 2010). The main chemical
75 structure of fumonisins is a diester of propane-1,2,3-tricarboxylic acid and a pentahydroxyicosane
76 containing a primary amino acid (Gurung et al., 1999). Due to their structural similarity to the lipid
77 sphingosine, the mechanism of action of fumonisins might include competition with sphingosine in
78 the sphingolipid metabolism (De Lucca, 2007; Riley et al., 1996).

79 The fumonisin B series, including FB₁, FB₂, FB₃, and FB₄, is the most toxic to plants and animals
80 (Abbas et al., 1998a). FB₁ is generally found in corn, rice, triticale, sorghum, beans, and asparagus.
81 It can cause equine leucoencephalomalacia and porcine pulmonary oedema (Scott, 2012). FB₁ has
82 been associated to human oesophageal cancer in humans (Chu and Li, 1994; Sydenham et al.,

83 1990). FB₂ is found often in lower concentrations than FB₁. Although FB₁ is the primarily studied
84 fumonisin, FB₂ is considered 3 to 4 times more cytotoxic than FB₁ (Dombrink-Kurtzman et al.,
85 1994).

86 Fumonisin biosynthetic (*FUM*) gene clusters were reported in *F. verticillioides*, *F. proliferatum*,
87 and *Fusarium oxysporum* (Proctor et al., 2003; Proctor et al., 2008; Waalwijk et al., 2004). The
88 gene *FUM1* encodes a polyketide synthase (PKS) necessary for the production of fumonisins,
89 which catalyses the initial steps in fumonisin biosynthesis (Bojja et al., 2004). Interestingly, the
90 flanking regions of the fumonisin cluster are not significantly similar between *Fusarium* spp.,
91 suggesting an independent species acquisition of the cluster (Proctor et al., 2008). It is not yet clear
92 how the sequence divergence within the cluster affects the fumonisin biosynthesis, but it was
93 evidenced that a single-point mutation can cause the occurrence of a nonproduction phenotype
94 (Proctor et al., 2006). Beside the *FUM* cluster, other genes are involved in fumonisin biosynthesis.
95 *FfVell* and *FfLae1*, components of a velvet-like complex, and *FvVE1* co-regulate the biosynthesis
96 of the fumonisins in *F. fujikuroi* and *F. verticillioides*, respectively (Myung et al., 2009; Wiemann
97 et al., 2010). *WcoA*, a component of a white collar photoreceptor family, *Ffg1* and the cAMP-
98 mediated signalling pathway affect other secondary metabolite pathways in *F. fujikuroi* (Estrada
99 and Avalos, 2008; Studt et al., 2013).

100 Fungi are microorganisms exposed to environmental stimuli on a circadian rhythm, such as
101 temperature, light, and humidity. During the evolution, they developed complex genetic
102 mechanisms to respond to those environmental variables. Light affects fungal growth, reproduction
103 and pigment biosynthesis, depending on the species (Rodriguez-Romero et al., 2010). Recently, it
104 has been found that light also affects the secondary metabolism of fungi, particularly the mycotoxin
105 production. Regarding the light-sensing function in fungi, many fungal species use a number of
106 various wavelength-specific receptors. Wavelengths from both sides of the spectrum (blue and red)
107 had the strongest inhibitory effect on ochratoxin A production compared to the dark control in
108 *Aspergillus niger* (Schmidt-Heydt et al., 2011). *Penicillium expansum* increased the production of

109 citrinin under white, red and blue light, whereas *Penicillium verrucosum* stimulated citrinin
110 production under yellow and green light (Schmidt-Heydt et al., 2011). Wavelengths within the
111 visible spectrum (from red to blue) increased the fumonisin biosynthesis compared to darkness in
112 two species of *Fusarium* originating from maize, in particular red and blue light in *F. proliferatum*,
113 and red and royal blue light in *F. verticillioides* (Fanelli et al., 2012a; 2012b).

114 The aim of our study was to investigate the fumonisin biosynthesis and *FUM1* relative
115 expression in different light conditions between three *Fusarium* species (*F. fujikuroi*, *F.*
116 *verticillioides*, and *F. proliferatum*) originated from rice and to compare their pathogenicity.

117

118 **2. Materials and methods**

119

120 *2.1. Fungal strains*

121

122 Fungal strains of *F. fujikuroi* (Augusto2), *F. verticillioides* (19-115), and *F. proliferatum* (19-
123 113), isolated and characterized from Italian bakanae-associated rice samples (Amatulli et al., 2010)
124 were used in this study. Three additional bakanae-associated isolates (I1.3 and CSV1 of *F. fujikuroi*,
125 and 11-471 of *F. proliferatum*) from Northern Italy were included in this study. Reference
126 *Fusarium* rice strains from other countries obtained from the Fusarium Research Centre
127 (Pennsylvania State University, USA) were also used: *F. fujikuroi* M-1149 from Taiwan, *F.*
128 *verticillioides* M-5331 from China, and *F. proliferatum* M-6580 from Thailand (Table 1). The
129 strains were stored at 4 °C in Spezieller nährstoffarmer agar (0.2 g sucrose, 0.2 g glucose, 1.0 g
130 KNO₃, 1.0 g KH₂PO₄, 0.5 g MgSO₄ · 7H₂O, 0.5 g NaCl, and 12 g agar per litre).

131

132 *2.2. DNA extraction and EF-1 α /FUM1 amplification*

133

134 Total DNA of nine fungal strains was extracted with the NucleoSpin Plant II kit (Macherey-
135 Nagel, Düren, Germany) from mycelium grown on potato dextrose agar (PDA, Merck KGaA,
136 Darmstadt, Germany) plates according to the manufacturer's instructions. Twenty ng of fungal
137 DNA were used for the PCR reaction performed with a mixture containing 10X PCR buffer
138 (Qiagen, Düsseldorf, Germany), 0.5 μ M of each primer, 0.5 mM of dNTPs (Qiagen), 2 U Taq DNA
139 polymerase (Qiagen) and the final volume adjusted to 40 μ l with sterile distilled water. Three
140 *Fusarium* isolates (I1.3, CSV1, and 11-471) not characterized by Amatulli et al. (2010) were
141 amplified in the portion of the *EF-1 α* gene by using specific primers (O'Donnell et al., 1998b).
142 Fum1F1 and Fum1R2 primers were used for the amplification of a part of the *FUM1* gene in the
143 nine strains (Stępień et al., 2011). The PCR program was initiated with a denaturation step of 94° C
144 for 5 min, followed by 35 cycles at 94 °C for 45 sec, 55 °C for 45 sec, and 72 °C for 2 min, and a
145 final extension step of 7 min at 72 °C.

146

147 2.3. Sequence analysis

148

149 *EF-1 α* and *FUM1* amplicon sequences were deposited in GenBank (Table 1) and comparison
150 with sequences available was done by using the BLAST program (www.ncbi.nlm.nih.gov).
151 Multiple sequence alignment of nucleotide (nt) and amino acid (aa) sequences and identification of
152 open reading frames were done by using the program AlignX (Vector NTI Suite V 5.5, InforMax,
153 North Bethesda, Maryland, USA) with the Clustal W algorithm (Thompson et al., 1994).
154 Phylogenetic analyses were performed using MEGA 5 (Tamura et al., 2011). Neighbor-joining (NJ)
155 trees were constructed with 1,000 bootstrap replications.

156

157 2.4. Selection of growing medium

158

159 Fungal cultures were subcultured on PDA plates for 10 days at 20 °C. A spore suspension of the
160 strains was prepared from the plates in sterile distilled water. One hundred μl of a 10^6 spores ml^{-1}
161 solution was inoculated in 50 ml of three growing media: (a) potato dextrose broth (PDB, Merck
162 KGaA), (b) Czapek-Dox broth (Sigma-Aldrich, Buchs, Switzerland), and (c) GYAM (0.24 M
163 glucose, 0.05% yeast extract, 8.0 mM L-asparagine, 5.0 mM malic acid, 1.7 mM NaCl, 4.4 mM
164 K_2HPO_4 , 2.0 mM MgSO_4 , and 8.8 mM CaCl_2), by shaking at 100 rpm for 10 days in darkness.
165 Growing media were evaluated for their efficiency for induction of fumonisin production in
166 different *Fusarium* strains. The best fumonisin-producing medium was selected for the tests of light
167 conditions and pathogenicity, as described below. The experiment was carried out three times at
168 constant temperature.

169

170 2.5. Light conditions

171

172 *Fusarium* strains were grown in PDB under different light conditions: red (685 nm), yellow
173 (580 nm), green (535 nm), blue (475 nm), and white. In addition, the growth under dark and
174 light/dark alternation were examined. To investigate the influence of light and various wavelengths,
175 the growth chambers were provided with a lighting system containing five RoHs comforted bulbs.
176 Each bulb contained 36 Light Emitting Diodes (Super Bright LEDs Inc., St. Louis, USA) that
177 emitted at corresponding wavelengths as indicated above. The bulbs were fixed at the four corners
178 and in the middle of the upper side of the chambers, and were kept at a 20 cm distance from the
179 orbital shaker where fungal strains were grown for 10 days at 100 rpm. Only one chamber was not
180 provided with the lighting system, and it was used as a dark control. The luminous flux of each bulb
181 was 72 lumen, and the light intensity was 4.0 lumen/cm^2 or 76 mW/cm^2 on the fungal culture.
182 Continuous light or dark was applied in the chambers for each experiment, with the exception of the
183 growth under light/dark (12 h: 12 h). The experiments were carried out three times at constant
184 temperature of 20 °C maintained by the control system of the growth chambers.

185

186 *2.6. Fumonisin analysis*

187

188 For fumonisin quantification, the strains grown in PDB were filtered through sterile cheese cloth
189 (Merck KGaA) to separate the supernatant and the mycelia. The supernatant was used for FB₁ and
190 FB₂ analyses, whereas the mycelium was used for subsequent RNA extraction and obtainment of
191 the dry mycelium described as follows. The collected mycelium was weighed and divided into two
192 equal parts. One part was immediately processed for RNA extraction, and the other part was dried
193 at 70 °C for 24 h to measure the mycelial dry weight, that was multiplied by two (including also the
194 mycelium used for RNA extraction) to obtain the total dry mycelium. The total dry mycelium was
195 used to normalize the final FB₁ and FB₂ values obtained as described below.

196 The recovered supernatant was additionally filtered through regenerated cellulose 0.45 µm filter
197 and analysed by HPLC coupled with a triple quadrupole mass spectrometer. Liquid chromatography
198 was performed with Varian Model 212-LC micro pumps (Hansen Way, CA, USA) coupled with a
199 Varian 126 autosampler Model 410 Prostar. A Synergi 4u Fusion-RP 80A (100 mm x 2.0 mm,
200 Phenomenex, Castel Maggiore, Italy) analytical column was used coupled with Fusion-RP (4 x 2.0
201 mm) security guard for LC separation. The chromatographic conditions were: column temperature
202 at 45 °C; mobile phase consisting of eluent A (buffer solution with 20 mM ammonium formate-
203 formic acid at pH 3.75) and eluent B (methanol), using a flow rate of 0.3 ml/min. A gradient elution
204 was applied as follows: 0 min 30% B; 0.1-5 min 30-90% B; 5.1-10 min 90-30% B. Five minutes of
205 post run were necessary for column conditioning before the subsequent injection. The injection
206 volume was 10 µl.

207 The triple quadrupole mass spectrometer (Varian 310-MS) was operated in the negative/positive
208 electrospray ionization mode (ESI/ESI⁺). To select the MS/MS parameters for the analysis of
209 fumonisins by multiple reaction monitoring (SRM), ESI mass spectra for each analyte were initially
210 analysed introducing the stock fumonisin standard solution (Sigma-Aldrich) with direct injection

211 into the spectrometer by a Harvard 11 plus infusion pump. The m/z 706 positive ion and m/z 720.4
212 negative ion were used, respectively, as parent ions for FB₁ and FB₂. The most intense daughter
213 ions, resulting from collision-induced dissociation with argon, used to detect and quantify the
214 fumonisin content were: m/z 336 at 36 eV of collision energy (CE) and 318 at 318 eV for FB₁; m/z
215 156.7 at 30 eV CE and 562.4 at 16.5 eV for FB₂. The limits of detection (LOD; signal-to-noise
216 ratio: 3) and quantification (LOQ; signal-to-noise ratio: 10) were, respectively, 0.62 µg/l and 1.55
217 µg/l for FB₁, 2.09 µg/l and 5.17 µg/l for FB₂. Each analysis was performed in triplicate.

218

219 2.7. RNA extraction, reverse transcription and real-time PCR for *FUM1*

220

221 Total RNA of fungi was extracted from mycelium with Aurum Total RNA fatty and fibrous
222 tissue kit (Bio-Rad, Richmond, CA, USA). Total RNA was DNase treated using TURBO DNase
223 (Ambion, Foster City, CA, USA) according to the manufacturer's instructions to remove
224 contaminating DNA, and then subjected to reverse transcription using the High capacity cDNA
225 reverse transcription kit (Applied Biosystems, Foster City, CA, USA). The cDNA mixture
226 contained the total RNA (ranging from 0.1 to 1000 ng), 2 µl 10X RT buffer, 0.8 µl 25X dNTP mix,
227 2 µl 10X RT random primers, 1 µl Multiscribe™ reverse transcriptase, and 1 µl RNase inhibitor in a
228 total volume of 20 µl. cDNA synthesis conditions were: 10 min at 25 °C, 120 min at 37 °C, and 5
229 min at 85 °C. The resulting cDNA was used as a template for real-time PCR.

230 Real-time PCR was used for the quantification of the *FUM1* transcript expression under different
231 light conditions. Primers for *FUM1* gene sequence were designed: Fum1fp1 (5'-
232 AGGATTGGCTGGATCTTCAC-3') and Fum1fp2 (5'-TAATACGGTTGGAAATGGCA-3') for
233 *F. fujikuroi* and *F. proliferatum* on the basis of the GenBank accession no. AY577454 (nt position
234 149-241) giving an amplicon of 93 bp, and Fum1univs (5'- CCAGCTGTTTTTCCCTGCTA-3')
235 and Fum1univa (5'- CGATTTCCCATCAGCAAGAT-3') for *F. verticillioides* designed from the
236 sequence AF155773 (nt position 25785-25868) giving an amplicon of 103 bp. PCR conditions were

237 as follows: an initial step at 95 °C for 5 min, and 40 cycles at 95 °C for 15 s (denaturation), 60 °C
238 for 30 s (annealing), and 72 °C for 30 s (extension). The reactions were carried out in an iCycler
239 (Bio-Rad) and contained 1 µl cDNA, 10 µl SsoFast™ EvaGreen® Supermix 2X (Bio-Rad), 2.5 mM
240 each primer in a total volume of 20 µl. PQTUB-F and PQTUB-R primers designed from the
241 sequence of the β-tubulin gene *tub2* were used as a control for the constitutive expression (Glass
242 and Donaldson, 1995). To investigate the range of concentrations where the target RNA and C_T
243 values were linearly correlated, and to determine the reaction efficiency for both sets of *FUM1*
244 primers, the reactions were performed by using the cDNA synthesized from serially diluted RNAs.
245 Baseline range and C_T values were automatically calculated using the iCycler Optical System
246 Software v. 3.0. The expression of the *FUM1* gene was normalized to that of *tub2*, by subtracting
247 the *tub2* C_T value from the C_T value of the *FUM1* gene resulting from the ΔC_T. The expression ratio
248 was calculated from equation $2^{-\Delta\Delta C_T}$, where ΔΔC_T represents the ΔC_{Tsample} – ΔC_{Tcontrol} (Livak and
249 Schmittgen, 2001).

250

251 2.8. Pathogenicity tests

252

253 Fungal strains were cultured in PDB for 10 days in darkness in acclimatized chamber at 20 °C.
254 The strains were filtered through sterile cheese cloth to a final spore concentration of 10⁶ ml⁻¹ in
255 sterile distilled water. The rice cultivar Galileo susceptible to *F. fujikuroi* was used for
256 pathogenicity tests. Rice seeds were surface-disinfected in 1% sodium hypochlorite for 2 min and
257 rinsed in sterile distilled water. A total of 120 seeds were soaked in 100 ml spore suspension by
258 shaking for 30 min at room temperature. Control seeds were soaked in sterile distilled water. Seeds
259 were sown in plastic pots (40 x 24 x 12 cm) in triplicate (40 seeds per pot) in a sterile mixture of
260 peat and sand (60% : 40%). The plants were kept in greenhouse conditions (25 °C day : 17 °C
261 night) by watering 3 times per day. Disease symptoms were evaluated 30 days after germination.

262 We searched for bakanae symptoms including thin and elongated internodes typical of *F. fujikuroi*,
263 and for other less specific symptoms, such as chlorosis, necrosis and delayed growth.

264

265 2.9. Statistical analysis

266

267 Data from all the experiments were submitted to analysis of variance (ANOVA) by using the
268 Statistical Package for Social Science (SPSS, IBM, Chicago, IL, USA) version 17.0. The statistical
269 significance was judged at $P < 0.05$. Statistically significant differences among light treatments with
270 a reference to the dark incubation were determined by the *t* test. Pearson's correlation coefficient
271 between expression levels of *FUM1* gene and FB₁ content was also calculated.

272

273

274 3. Results

275

276 3.1. Species identification

277

278 The nine isolates of *Fusarium* spp. originated from rice were identified through analysis of the
279 *EF-1 α* and *FUM1* sequences (Table 1). Both genes permitted to identify four strains of *F. fujikuroi*,
280 three strains of *F. proliferatum* and two strains of *F. verticillioides*. The phylogenetic studies of the
281 *FUM1* gene portion (amplicons from 1030 to 1039 nt) allowed the separation of the three *Fusarium*
282 species similarly to those performed with the *EF-1 α* portion (amplicons from 649 to 661 nt). Thus,
283 phylogenetic analyses of the nucleotide (Supplementary Fig. 1) or amino acid (data not shown) of
284 the *EF-1 α* and *FUM1* fragments grouped the *Fusarium* strains into two clusters; one cluster
285 contained the strains of *F. fujikuroi* and *F. proliferatum*, and the another one the strains of *F.*
286 *verticillioides*. The first cluster was further divided into two subclusters allowing the separation of

287 *F. fujikuroi* and *F. proliferatum*. On the basis of the results obtained, *FUM1* gene sequence,
288 corresponding to the acetyltransferase domain of the PKS protein, could be used to differentiate
289 species of the *Gibberella fujikuroi* species complex. *F. fujikuroi* and *F. proliferatum* had 91.1%
290 *FUM1*-nucleotide sequence identity. A lower nucleotide identity was found when *F. verticillioides*
291 strains were compared to the strains of *F. proliferatum* and *F. fujikuroi* (77.3% and 78.7%,
292 respectively).

293

294 3.2. Selection of growing medium

295 The medium which allowed the highest production of FB₁ (Fig. 1 and Supplementary Table
296 1) and FB₂ (data not shown) in three *Fusarium* species was PDB. It induced 3.2 to 5.0 times higher
297 FB₁ production compared to the GYAM medium. Czapek-Dox was not a satisfactory growing
298 medium for the production of fumonisins since it allowed very low production of FB₁ in only two
299 *Fusarium* strains. On the basis of these results, lighting and pathogenicity tests were performed by
300 using PDB as a growing medium.

301

302 3.3. Fumonisin production in three *Fusarium* species under dark

303

304 Strains belonging to three *Fusarium* species were compared for fumonisin production after their
305 growth in dark. The highest FB₁ producing strains were *F. verticillioides* M-5331, *F. fujikuroi*
306 Augusto2, and *F. fujikuroi* M-1149 (Table 2). The other *Fusarium* strains showed lower FB₁
307 production. FB₂ biosynthesis was obtained in both strains of *F. verticillioides*, and in two out of four
308 strains of *F. fujikuroi* (I1.3 and Augusto2), while none of the *F. proliferatum* strains produced FB₂.
309 Interestingly, *F. verticillioides* M-5331 and 19-115, and *F. fujikuroi* I1.3 produced more FB₂ than
310 FB₁ (16.7, 17.3 and 25.9 times more, respectively).

311 By considering the geographic origin of the *F. verticillioides* strains, the M-5331 strain
312 originating from China produced 2.3 and 2.2 times more FB₁ and FB₂, respectively, than the Italian

313 strain 19-115 (Table 2). *F. fujikuroi* Augusto2 originating from Italy was a higher FB₁/FB₂ producer
314 compared to the Taiwanese strain of *F. fujikuroi* (M-1149). The Italian strain of *F. proliferatum*
315 (11-471) showed higher level of FB₁ production compared to the Thai strain (M-6580).

316

317 3.4. Fumonisin production in different light conditions

318

319 All the species of *Fusarium* isolated from rice showed a higher production of fumonisins (Fig. 2
320 and Table 2) under different light conditions compared to darkness. *F. proliferatum* strains had the
321 highest FB₁ increase under white and blue light, and under light/dark. Red, green and yellow light
322 were also stimulating the FB₁ biosynthesis compared to the dark incubation. FB₁ production was
323 highly stimulated in both strains of *F. verticillioides* under yellow and green light. The other light
324 conditions also activated the FB₁ production in *F. verticillioides*, but to a lower extent. *F. fujikuroi*
325 Augusto2 and M-1149 stimulated the FB₁ biosynthesis under white and blue light, and light/dark.
326 The other two strains of *F. fujikuroi* (I1.3 and CSV1) ceased FB₁ production under different
327 wavelengths and light conditions, with the exception of blue light and the light/dark alternation
328 (Fig. 2 and Table 2). Conclusively, the highest production of FB₁ was obtained in *F. fujikuroi* strain
329 M-1149 (white) and *F. verticillioides* M-5331 (yellow light).

330 FB₂ production was activated by different wavelengths of light; red and blue light in the three
331 strains of *F. proliferatum* and in *F. fujikuroi* Augusto2 and M-1149. It was also stimulated under
332 light/dark alternation in *F. proliferatum* and most *F. fujikuroi* strains. Red and yellow light activated
333 FB₂ biosynthesis in *F. verticillioides* (Table 2 and Supplementary Fig. 2). Red light induced a
334 higher FB₂ production compared to FB₁ in both strains of *F. verticillioides* (Table 2).

335 We observed that the light-pattern of fumonisin synthesis was generally more similar between *F.*
336 *fujikuroi* and *F. proliferatum*, compared to *F. verticillioides*. Additionally, a stimulation of
337 mycelium production was also observed under different light conditions compared to the dark
338 incubation in all three *Fusarium* species (Supplementary Fig. 3). All light conditions that we

339 applied (light of different wavelengths, white light and the light/dark alternation) had a significant
340 effect on the mycelium production with respect to dark after 10 days of growth in PDB.

341

342 3.5. Expression of the *FUM1* gene in different light conditions

343

344 Ct values and the logarithm of RNA concentrations ranging from 1000 to 0.1 ng were linearly
345 correlated for both sets of *FUM1* primers. An average squared regression (R^2) of 0.998 and a
346 reaction efficiency of 97.5% were obtained for the *FUM1* primer pair designed for *F. fujikuroi* and
347 *F. proliferatum*, while similar values of 0.999 (R^2) and 97.8% (reaction efficiency) were obtained
348 for the *FUM1* primer pair for *F. verticillioides*. These results allowed the use of both set of primers
349 in the subsequent real-time PCR reactions to investigate the light influence.

350 The *FUM1* expression was activated under different light conditions in all three species of
351 *Fusarium* from rice compared to the dark. It was highly activated under blue, and white light, and
352 light/dark alternation in *F. proliferatum* and *F. fujikuroi* strains Augusto2 and M-1149, but it was
353 also activated under green light in *F. proliferatum*, and under red light in *F. fujikuroi* Augusto2 and
354 M-1149 (Fig. 3). The other two strains of *F. fujikuroi* (I1.3 and CSV1) showed significant *FUM1*
355 expression only under blue light and light/dark alternation. Wavelengths that highly stimulated
356 *FUM1* expression in *F. verticillioides* were yellow and green.

357 The highest increase was observed in *F. fujikuroi* M-1149 (486-fold change; white), *F. fujikuroi*
358 Augusto2 (384-fold change; white light) and *F. proliferatum* 11-471 (267-fold change; blue light)
359 (Table 2). The *FUM1* expression level was found in correspondence with FB_1 production and the
360 value for the Pearson's correlation coefficient was 0.78 for all three species. When the Pearson's
361 correlation coefficient was calculated for each species separately, a higher correlation was found in
362 *F. verticillioides* (0.97) and *F. fujikuroi* (0.80) compared to *F. proliferatum* (0.57).

363

364 3.6. Pathogenicity tests

365

366 Five of the 9 tested strains showed to be pathogenic for rice: *F. fujikuroi* M-1149, I1.3, and
367 CSV1 showed typical bakanae symptoms with a death incidence of 93%, 91%, and 83%,
368 respectively, while *F. verticillioides* M-5331 and 19-115 caused chlorotic leaves and delayed
369 growth with no death incidence (about one month after germination). Comparing the two *F.*
370 *verticillioides* strains, strain M-5331 caused a higher incidence of leaf chlorosis and plant stunting
371 than 19-115 (Table 3 and Fig. 4). On the other hand, one strain of *F. fujikuroi* (Augusto2) and all
372 three strains of *F. proliferatum* showed to be asymptomatic for the plants. Comparing pathogenic *F.*
373 *fujikuroi* and *F. verticillioides* strains, it can be observed that they influenced the growth of the
374 plants differently; *F. fujikuroi* with a plant internode elongation, and *F. verticillioides* with stunting.
375 Both growth ways affected negatively the general plant behaviour, but plant death occurred only
376 when the plant underwent a rapid elongation.

377

378 **Discussion**

379 There are reports of natural contamination of rice with fumonisins from Korea (Chung and Kim,
380 1995), United States (Abbas et al., 1998b), China (Trucksess, 2000), Brazil (Mallmann et al., 2001),
381 Argentina (Lerda et al., 2005), Japan (Kushiro et al., 2008), and Thailand (Tansakul et al., 2012). A
382 huge number of samples of rice plants and rice food products were analysed, and no fumonisin
383 contamination was found in Italian samples (data not published).

384 For this reason, fumonisins were measured from fungal strains grown *in vitro* in PDB, which was
385 previously selected. In general, there is limited information on the use of PDB as a growing medium
386 for mycotoxin production (Spadaro et al., 2010). We know that secondary metabolites, such as
387 gibberellins and bikaverin in *F. fujikuroi*, and fumonisins in *F. verticillioides*, are repressed by high
388 amounts of nitrogen (Mihlan et al., 2003; Schönig et al., 2008; Kim and Woloshuk, 2008). In this
389 work, the PDB medium non-supplemented with additional nitrogen sources showed to have
390 favourable nitrogen conditions for fumonisin production in comparison with other previously used

391 substrates, including GYAM and Czapek-Dox that contained other nitrogen sources (Proctor et al.,
392 2008; Amatulli et al., 2012).

393 *F. fujikuroi* Augusto2 was asymptomatic in pathogenicity tests on rice, but it showed a high
394 fumonisin-producing ability. On the contrary, another high fumonisin-producing strain (M-1149)
395 and two low fumonisin-producing strains (I1.3, and CSV1) of *F. fujikuroi* were more aggressive on
396 rice with hyper-elongation of the stems. This divergence may be related to the previous findings
397 showing that other components besides mycotoxins, such as phytohormones may influence the
398 pathogenicity of *F. fujikuroi* on rice (Wulff et al., 2010). Taking into consideration two other
399 species of *Fusarium*, we found a higher level of production of fumonisins in *F. verticillioides* which
400 showed pathogenicity on rice, while the fumonisin-producing strains of *F. proliferatum* were
401 asymptomatic. In *F. verticillioides*, the M-5331 strain from China induced a higher incidence of rice
402 stunting and a more abundant synthesis of fumonisins than the strain 19-115 from Italy. Stunted
403 growth could be associated with the inability of *F. verticillioides* to produce gibberellin, therefore
404 other factors might be causing the symptoms observed.

405 In this study, we showed for the first time the influence of light on fumonisin production in
406 isolates of *F. fujikuroi*, *F. proliferatum*, and *F. verticillioides* from rice. Fumonisin production was
407 considered to be higher during dark incubation, so most previous studies were performed by
408 growing fumonisin producing isolates in the dark (Alberts et al., 1990; Desjardins et al., 2000;
409 Wulff et al., 2010). However, recent findings indicated that light and different wavelengths of light
410 might have a stimulatory effect on fumonisin production in *F. verticillioides* and *F. proliferatum*
411 from maize compared to the dark incubation (Fanelli et al., 2012a; 2012b). Our data showed that
412 dark incubation induced fumonisin synthesis in all tested *Fusarium* species from rice, but the light
413 conditions were more stimulating for fumonisin production.

414 *F. fujikuroi* is reported to produce little or no fumonisin compared to *F. verticillioides* and *F.*
415 *proliferatum* (Desjardins et al., 2000; Stępień et al., 2011; Wulff et al., 2010). Here we report for the
416 first time that two strains of *F. fujikuroi* from rice have the ability to produce fumonisin levels

417 comparable to those of *F. verticillioides* and *F. proliferatum*. FB₁ and FB₂ production was highly
418 increased under white light in *F. fujikuroi* Augusto2 and M-1149. In these conditions, *F. fujikuroi*
419 Augusto2 from Italy and M-1149 from Taiwan proved to be the most abundant fumonisin
420 producers.

421 Many fungal species use specific wavelength receptors and all receptors contain an organic
422 molecule of low molecular weight, such as flavin, retinal or tetrapyrrols for blue-, green-, or red-
423 light perception, respectively (Rodriguez-Romero et al., 2010). Red-light sensing of fungi was
424 involved in sporulation and mycotoxin synthesis. In *Botrytis cinerea*, a red-light reversible
425 photoreaction was found in the recovery from the blue-light inhibition of sporulation (Tan, 1974).
426 *P. expansum* produced a high quantity of citrinin under red, blue and white light, whereas *P.*
427 *verrucosum* did so under yellow and green light (Schmidt-Heydt et al., 2011). Fanelli et al. (2012a;
428 2012b) found that the visible spectrum from red to blue increased fumonisin production in *F.*
429 *proliferatum* and *F. verticillioides* originated from maize.

430 As far as we know, little is known about the light wavelength sensing in fumonisin production of
431 *F. fujikuroi*. We reported here that white light, followed by blue light and light/dark alternation had
432 a strong stimulatory effect on FB₁ or FB₂ synthesis in two *F. fujikuroi* strains (Augusto2 and M-
433 1149). Under white light, FB₁ and FB₂ productions were increased, respectively, 75 and 15 times in
434 *F. fujikuroi* Augusto2, and 326 and 1367 times in *F. fujikuroi* M-1149. Our data indicated that a
435 better effectiveness of fumonisin production in *F. fujikuroi* was generally obtained with light
436 regimes compared to darkness. Positive influence of white light on fumonisin-producing profile was
437 found, and the result is in agreement with increase of production of secondary metabolites in other
438 organisms such as DON in *Fusarium graminearum*, citrinin in *P. expansum*, and aflatoxins in
439 *Aspergillus parasiticus* (Bennett et al., 1981; Schmidt-Heydt et al., 2011). The activation of
440 fumonisin biosynthesis found by light-dark alternation, may be attributed to the night-day cycle of
441 fungi. Many fungal species possess a circadian clock which is influenced by light and temperature
442 (Dunlap and Loros, 2006). Other two *F. fujikuroi* strains (I1.3 and CSV1) did not show an

443 activation in fumonisin production with light application, with the exception of light/dark
444 alternation (6 and 10 times FB₁ increase) and blue light (6 and 11 fold increase). It would be
445 interesting to study the expression of genes involved in fumonisin production, such as the *FUM*
446 cluster, the white collar gene, and the velvet-like complex, in low and high fumonisin-producing *F.*
447 *fujikuroi* strains.

448 Concerning *F. proliferatum*, white and blue light stimulated the FB₁ synthesis, whereas the FB₂
449 production was activated under red light and the light/dark alternation compared to darkness. Our
450 data fit with Fanelli et al (2012a), but we found additional induction of fumonisin biosynthesis
451 under white light and light/dark alternation. Strains of *F. proliferatum* showed 11 to 32 times more
452 FB₁ production under blue light, and 19 to 36 times more FB₂ production under red light.

453 Our data showed that different wavelengths, particularly yellow and green light, favour
454 fumonisin production in *F. verticillioides*. These wavelengths were also found stimulatory in the
455 previous work of Fanelli et al. (2012b). In our work, both strains of *F. verticillioides* showed 47 to
456 171 times more synthesis of FB₁ under yellow light, and 17 to 20 fold increase under green light in
457 comparison to darkness.

458 FB₂ production was higher compared to FB₁ in most strains of the three *Fusarium* species under
459 light/dark alternation, and in both strains of *F. verticillioides* under red light and dark. *Fusarium*
460 isolates able to produce more FB₂ than FB₁ have been already reported (Musser and Plattner, 1997),
461 and it could be possible that some light conditions are more favourable for FB₂ production, by
462 inducing a higher expression of *FUM2* gene, involved in the switch from FB₁ to FB₂ (Proctor et al.,
463 2003).

464 In conclusion, *F. fujikuroi* and *F. proliferatum* showed a similar light-regulation profile of
465 fumonisin biosynthesis that could be associated with their closely related phylogenetic relationship
466 within *Gibberella fujikuroi* species complex (Amatulli et al., 2010; Hsuan et al., 2011). On the other
467 hand, *F. proliferatum* and *F. verticillioides* showed different wavelength-regulation pattern for
468 fumonisin production which can be attributed to variability in phenotypic fumonisin biosynthesis

469 between these two species (Visentin et al., 2009). Indeed, *F. proliferatum* and *F. verticillioides*
470 exhibited different regulation profiles of fumonisin biosynthesis under different environmental
471 conditions, such as temperature and water stress (Marín et al., 2010).

472 Previous studies reported that *FUM1* gene expression showed a correlation with fumonisin
473 production, offering a diagnostic tool for the rapid and sensitive detection of metabolically active
474 fumonisin-producing *Fusarium* species (López-Errasquín et al., 2007; Jurado et al. 2010; Fanelli et
475 al., 2012a). In our work we also found a positive and high relationship between mRNA levels of
476 *FUM1* gene and FB₁ production. Some cases of lower correspondence between *FUM1* transcripts
477 and FB₁ content could be explained by slightly different time-points of transcription and mycotoxin
478 production.

479 Our results report fumonisin production and *FUM1* gene expression in members of the
480 *Gibberella fujikuroi* species complex isolated from rice. Fumonisin production was activated by
481 specific light conditions in three different *Fusarium* species. The variations have been found
482 between different *Fusarium* species, but a closer fumonisin-production profile was found between
483 *F. proliferatum* and *F. fujikuroi*, compared to *F. verticillioides*. Abundant and low fumonisin-
484 producing strains were found in *F. fujikuroi* under different light conditions. The data obtained in
485 this study highlight the need for a deeper analysis of fumonisin production in *F. fujikuroi*, the major
486 causal agent of the bakanae disease, and a re-examination of its mycotoxigenic capacity, which can
487 be additionally supported with recent information coming from the *F. fujikuroi* genomic and
488 transcriptomic data (Jeong et al., 2013; Wiemann et al., 2013).

489

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491

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496

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675 **Table 1**
 676 List of *Fusarium* strains used in this study.
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Strain	Species	Origin	Host	Accession no. (<i>EF-1α</i> gene)	Reference (<i>EF-1α</i> gene)	Accession no. (<i>FUM1</i> gene)	Reference (<i>FUM1</i> gene)
11-471	<i>F. proliferatum</i>	Italy	<i>Oryza sativa</i>	KC121066	This study	KC188784	This study
19-113	<i>F. proliferatum</i>	Italy	<i>Oryza sativa</i>	GQ848533	Amatulli et al., 2010	KC188785	This study
M-6580	<i>F. proliferatum</i>	Thailand	<i>Oryza sativa</i>	JN092336	Amatulli et al., 2010	KC188786	This study
19-115	<i>F. verticillioides</i>	Italy	<i>Oryza sativa</i>	GQ848530	Amatulli et al., 2010	KC188787	This study
M-5331	<i>F. verticillioides</i>	China	<i>Oryza sativa</i>	AY337449	Yergeau et al., 2005	KC188788	This study
I1.3	<i>F. fujikuroi</i>	Italy	<i>Oryza sativa</i>	GQ848523	Amatulli et al., 2010	KC188789	This study
CSV1	<i>F. fujikuroi</i>	Italy	<i>Oryza sativa</i>	KC121067	This study	KC188790	This study
Augusto2	<i>F. fujikuroi</i>	Italy	<i>Oryza sativa</i>	KC121068	This study	KC188791	This study
M-1149	<i>F. fujikuroi</i>	Taiwan	<i>Oryza sativa</i>	HM243234	Amatulli et al., 2010	KC188792	This study

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Table 2

Relative expression of FUM1 gene (FC), and FB₁ and FB₂ production (µg per g of mycelial dry weight) of *Fusarium* strains grown under different light conditions.

<i>F. proliferatum</i>												
	11-471			19-113			M-6580					
	FUM1	FB ₁ (µg / g)	FB ₂ (µg / g)	FUM1	FB ₁ (µg / g)	FB ₂ (µg / g)	FUM1	FB ₁ (µg / g)	FB ₂ (µg / g)	FUM1	FB ₁ (µg / g)	FB ₂ (µg / g)
Red	1.77±0.21	43±4.0	24±1.9	1.28±0.06	36±3.6	36±2.9	1.78±0.17	29±3.2	19±2.3			
Yellow	2.33±0.13	27±2.2	ND*	2.23±0.22	30±4.1	ND	1.96±0.16	48±3.3	ND			
Green	3.64±0.44	128±9.2	9±1.6	3.13±0.51	56±4.2	ND	2.43±0.31	43±3.0	ND			
Blue	267±21.16	214±20.8	22±0.9	253±22.31	289±25.7	15±1.4	194±21.07	290±32.1	21±2.5			
White	10.73±1.09	412±52.9	ND	5.63±0.72	159±18.1	ND	7.38±0.64	286±30.4	ND			
Light/Dark	4.56±0.54	145±11.9	320±35.5	9.42±0.68	201±24.2	489±50.4	5.92±0.71	249±30.5	276±21.6			
Dark	1±0.15	20±1.8	ND	1±0.14	12±1.3	ND	1±0.10	9±0.7	ND			

<i>F. verticillioides</i>						
	19-115			M-5331		
	FUM1	FB ₁ (µg / g)	FB ₂ (µg / g)	FUM1	FB ₁ (µg / g)	FB ₂ (µg / g)
Red	5.98±0.47	35±4.4	494±43.2	8.93±1.13	278±25.9	1694±139.2
Yellow	9.40±0.53	1029±149.6	435±38.2	185±23.64	8524±822.6	1930±185.3
Green	22.43±1.31	444±28.5	15±3.9	15.84±1.02	843±62.1	82±8.5
Blue	3.59±0.47	151±17.9	222±23.7	6.11±1.09	296±35.3	ND
White	1.22±0.09	27±3.1	ND	1.75±0.18	123±15.5	273±30.4
Light/Dark	3.81±0.49	162±18.4	225±23.3	6.02±1.08	272±30.1	393±42.9
Dark	1±0.11	22±2.9	380±30.1	1±0.20	50±6.2	834±92.9

<i>F. fujikuroi</i>												
	I1.3			CSV1			Augusto2			M-1149		
	FUM1	FB ₁ (µg / g)	FB ₂ (µg / g)	FUM1	FB ₁ (µg / g)	FB ₂ (µg / g)	FUM1	FB ₁ (µg / g)	FB ₂ (µg / g)	FUM1	FB ₁ (µg / g)	FB ₂ (µg / g)
Red	1.05±0.02	ND	ND	1.09±0.03	ND	ND	8.61±1.02	249±28.3	59±4.8	10.86±0.84	107±13.1	42±3.9
Yellow	1.19±0.11	ND	ND	1.22±0.13	ND	ND	1.73±0.13	64±5.5	17±6.8	1.22±0.15	68±6.6	ND
Green	1.09±0.09	ND	ND	1.14±0.11	ND	ND	1.19±0.07	59±3.4	ND	1.33±0.12	54±6.6	ND
Blue	4.32±0.27	39±3.6	ND	5.20±0.98	171±15.6	ND	20.8±1.76	346±40.2	46±3.7	23.47±1.28	404±44.8	58±4.9
White	1.12±0.09	ND	ND	1.25±0.08	ND	ND	383.78±34.29	3650±387.3	534±78.6	485.73±45.06	14002±1633.6	1367±80.0
Light/Dark	3.08±0.46	44±4.6	319±35.7	4.66±0.93	157±20.8	239±18.9	7.33±1.41	359±38.3	ND	2.08±0.16	130±10.9	185±23.1
Dark	1±0.14	7±1.2	181±24.1	1±0.15	16±2.1	ND	1±0.19	49±4.8	36±2.6	1±0.13	43±3.9	ND

*ND- not detected

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686 **Table 3**
 687 Pathogenicity tests of *Fusarium* strains on the rice cultivar Galileo.
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Strain	Germination (%)	Elongated plants with chlorotic leaves (%)	Stunted plants with chlorotic leaves (%)	Death incidence (%)
<i>F. proliferatum</i> 11-471	98	0	0	0
<i>F. proliferatum</i> 19-113	75	0	0	0
<i>F. proliferatum</i> M-6580	75	0	0	0
<i>F. verticillioides</i> 19-115	60	0	21	0
<i>F. verticillioides</i> M-5331	58	0	87	0
<i>F. fujikuroi</i> I1.3	83	91	0	91
<i>F. fujikuroi</i> CSV1	92	83	0	83
<i>F. fujikuroi</i> Augusto2	93	5	0	5
<i>F. fujikuroi</i> M-1149	52	93	0	93

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691 **Supplementary Table 1**692 FB₁ production (µg per g of mycelial dry weight) in *Fusarium* strains grown in different media under dark.

Isolate	FB ₁ production (µg / g)		
	PDB	Gyam	Czapek-Dox
<i>F. proliferatum</i> 11-471	22±4.21	6±0.52	ND ⁶⁹⁴
<i>F. proliferatum</i> 19-113	13±3.08	4±0.03	ND
<i>F. proliferatum</i> M-6580	10±2.07	3±0.02	ND ⁶⁹⁵
<i>F. verticillioides</i> 19-115	23±3.55	6±1.13	ND
<i>F. verticillioides</i> M-5331	52±7.08	13±1.54	3±0.20 ⁶⁹⁶
<i>F. fujikuroi</i> I1.3	8±1.03	2±0.16	ND
<i>F. fujikuroi</i> CSV1	17±3.06	5±0.34	ND
<i>F. fujikuroi</i> Augusto2	50±9.17	10±1.24	2±0.12 ⁶⁹⁷
<i>F. fujikuroi</i> M-1149	42±7.32	11±0.95	ND

698 * ND- not detected

699

700 **Figure captions**

701

702 **Fig. 1.** Production of FB₁ in strains of three *Fusarium* species: *F. proliferatum*, *F. verticillioides*,
703 and *F. fujikuroi* in three different growing media: PDB, Gyam and Czapek-Dox. Strains were
704 grown for 10 days by shaking (100 rpm) in darkness at 20 °C. Error bars show standard deviations
705 for triplicate assays.

706

707 **Fig. 2.** Production of FB₁ in strains of three *Fusarium* species: *F. proliferatum*, *F. verticillioides*,
708 and *F. fujikuroi* under different light conditions. Dark incubation was used as a reference. Strains
709 were grown in PDB for 10 days by shaking (100 rpm) at 20 °C. Error bars show standard deviations
710 for triplicate assays. Statistical significance: $P < 0.05$ for all comparisons.

711

712 **Fig. 3.** Relative expression of *FUM1* gene by real-time RT-PCR in strains of *F. proliferatum*, *F.*
713 *verticillioides*, and *F. fujikuroi* under different light conditions. Dark incubation was used as a
714 reference. Strains were grown in PDB for 10 days by shaking (100 rpm) at 20 °C. Error bars show
715 standard deviations for triplicate assays. Statistical significance: $P < 0.05$ for all comparisons.

716

717 **Fig. 4.** Symptomatology induced on 1-month old rice plants (cultivar Galileo) artificially inoculated
718 with *Fusarium* strains. The following *Fusarium* species were used for pathogenicity tests: *F.*
719 *fujikuroi* (1. I1.3; 2. M-1149; 3. CSV1; 4. Augusto2), *F. proliferatum* (5. 19-113; 6. 11-471; 7. M-
720 6580), and *F. verticillioides* (8. 19-115; 9. M-5331).

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722

723 **Supplementary Fig. 1.** Phylogenetic analyses based on the partial nucleotide sequences of *EF-1 α*
724 and *FUM1* genes from *Fusarium* strains: *F. fujikuroi* (I1.3, Augusto2, CSV1 and M-1149), *F.*
725 *proliferatum* (11-471, 19-113 and M-6580), and *F. verticillioides* (19-115 and M-5331). Reference
726 isolates of *F. fujikuroi* (HF679028), *F. proliferatum* (JF740718) and *F. verticillioides* (AB674289)
727 for *EF-1 α* gene, and *F. fujikuroi* (HF679031) and *F. verticillioides* (AF155773) for *FUM1* gene are
728 shown in bold. Phylogenetic analyses were performed by neighbor-joining method using MEGA 5
729 (Tamura et al., 2011). Bootstrap analyses were supported with 1,000 replications.

730

731 **Supplementary Fig. 2.** Production of FB₂ in strains of three *Fusarium* species: *F. proliferatum*, *F.*
732 *verticillioides*, and *F. fujikuroi* under different light conditions. Dark incubation was used as a
733 reference. Strains were grown in PDB for 10 days by shaking (100 rpm) at 20 °C. Error bars show
734 standard deviations for triplicate assays. Statistical significance: $P < 0.05$ for all comparisons.

735

736 **Supplementary Fig. 3.** Dry mycelium weight (g) of *Fusarium* strains grown at 20 °C under
737 different light conditions. Strains were grown in PDB for 10 days by shaking (100 rpm). Error bars
738 show standard deviations for triplicate assays.